

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/553,459  
Source: IFWP  
Date Processed by STIC: 1/19/07

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

**Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.**

**Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.**

**Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:**

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/553,459</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



do not include  
these headings. Do not include page numbers.

IFWP

see pp 1-4

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:18

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

see item 4 on  
Error summary  
sheet

W--> 1 WO 2004/092396  
W--> 2 PCT/US2004/011622  
4 <110> APPLICANT: Hallenbeck, Paul  
5 Hampton, Garret  
6 Hay, Carl  
7 Huang, Ying  
8 Jakubczak, John  
9 Phipps, Sandrina

W--> 10 <120> TITLE OF INVENTION: FLAP ENDONUCLEASE 1 (FEN1) REGULATORY SEQUENCES AND USES  
THEREOF

Does Not Comply  
Corrected Diskette Needed

12 <130> FILE REFERENCE: GTIN-021WO  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/553,459  
C--> 14 <141> CURRENT FILING DATE: 2005-10-17  
14 <150> PRIOR APPLICATION NUMBER: 60/463,148  
15 <151> PRIOR FILING DATE: 2003-04-15  
W--> 16 <160> NUMBER OF SEQ ID: 8  
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0

see item 2  
& on Error summary sheet

## ERRORED SEQUENCES

19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 2259  
21 <212> TYPE: DNA  
22 <213> ORGANISM: H. sapiens  
W--> 23 <400> SEQUENCE: 1  
24 catgcggta tcaaggagcc tggtgctgcc gtgaaacaga ggctgatttt agcccgaaaa 60  
25 ttagctgca gatcaatggc ccttattagc attttctgag gccaataatc tgaccactat 120  
26 gaaaacgtga ctaaaggatc gaactctctg cctgagaaaa accacataca agaaaaaagtt 180  
27 tgccatacaat ttccggagct ttgtggacca gtgtatatac acaccaagct gagaaccccc 240  
28 gctataagtc actgactgtt ggtacccaga tctcaatatac tttttttttt gacggagtct 300  
29 cattttttgg acggcgcttc actctgtcgc ccgggcttgg gggcagtggc acgatctcg 360  
30 ctcactgcaa cctctgcctc ccgggttcta gagattctca tacctcagcc tctcgagtag 420  
31 ctgggactat aggattacag gtgcgcacca ccacatctaa tttttgtatt ttttagtagag 480  
32 atggggtttt gccatgttgg ccaggatgtt cttgaattcc tgacctcagg tgatctgcct 540  
33 gcctcgccct cccaaagtac tgagattaca ggtgtgagtt gccgcgcaca ggctcaattt 600  
34 tttttttttt ccagacagtc ttgtctatc gcccaggctg gagtgcttgg agtgcagtgg 660  
35 tgccaaactcg gtcactgca agtccgcct tctgggttca agtgattatac ctgcctcagc 720  
36 ctcggagca gctgggatca cagggtgtgaa ccacatgcc cggctaaattt tttgtatattt 780  
E--> 37 taggagagac agggtttca cttgtctggcc aggtggat tgaacttctg acctctgtat 840  
38 ccgcctcgccct cagctccca aagtgtggg attacaggag tgaaccaccc cgcctggccc 900  
39 tcaatttcta attcgtatt ttctctacta cctatgtat tatggaaatc tggagat 960  
E--> 40 ggtcaagaca ttcaagttct ggttctgagt aatctgat tggataaaac gactgtataa 1020  
41 totatttcac agaactgaaa aataagaaaat atgatgaatc aaagcatcta gtgcctagca 1080

invalid  
nucleic acid  
designators

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/553,459**

DATE: 01/23/2007  
TIME: 16:44:18

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

42 ggtagtattt tgctcaacag gtatttgctt ccttcctaaq gctgttaggg agatgatgag 1140 → Invalid  
E--> 43 ataatgtctt ttatgaaaaga gggcttgtaa cgtaaagatc tgtacaatg ttaacttcat 1200  
44 tgtcacccgt cagccaatgc ttctaaaatc cagaacataa caactctaga gaagtaaact 1260  
45 gccccatttgc ttctgagaca ctggattca attcagtaaa caatcacggc ccccttcccc 1320  
46 caaaatgata aagacaatca ctgcccatttgc tttagcttcc aattacgggc cctctgttt 1380  
47 gcactgagaa tacaaagatg aatagacatc atcccagagc tagatgcgc tcagacgggt 1440  
48 gtcacttagga ggcgtggccg aaaacaaaaga agtccatgga acgtggccag agatctgtac 1500  
49 agaggctgtg ggcgtctcta ggaaagtctg gccaagtgc tgagagttgg aagtgtttca 1560  
50 ccaataaaca tttgcccagg gcattgttagg atgggcacgg gttcggcaga agaactttcc 1620  
51 aaataaagat aacacaccac cgataacaaa qataataaaa ctqqaqqta tccaaaatttc 1680 → Invalid  
E--> 52 gcccacggcc tctcgccctt agaaaatgcgg agctgagaaa cctaaggagt tcatggcaag 1740  
53 gggcttcccc cttccccacc cttcagccca agccggaggt tccaggagcg tctagccctc 1800  
54 tggatctccg gctctgagg agataacgcg ggtgtgggtc agacccggag gggtcctcgc 1860  
E--> 55 atctccgtt ggaactcccc tcaacgcgtt caccatttt ccccgcaag gtaatccgc 1920  
56 cgctccgcca cccgaagaac acgtcgacag gacggcgcg ctagcacaac cggaaaaggaa 1980  
57 agtccctccg gccaagtgg cattgaggga cttgtgttcc tgcatggcgtt ggttagagg 2040  
58 gagcaggggc ctggggggac ctgggtgtggg tggagtgggg acaaggcgtg gagaaggta 2100  
E--> 59 1  
E--> 60 wO 2004/092396  
E--> 65 Pct/us2004/01162  
E--> 66 2  
E--> 69 cggccagggtc gctgagagac tctgttctcc ctggagggac tggttgccat gagagcagcc 2160  
E--> 70 gtctgagggg acgcagccgt cactacgcgc cccaaagaggc tgtgcgtggc gacgggtca 2220  
E--> 71 cgtgacggga gcgccggctt tggaaaggcgg ctgaacgtc → 2259  
E--> 72 2259

see item 1 on Error Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:19

FYI  
Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

Invalid Line Length:  
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 71

10/553,459 4

<210> 8  
<211> 270

2

WO 2004/092396

PCT/US2004/011  
622

*delete*

<212> DNA

5  
VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/553,459

DATE: 01/23/2007  
TIME: 16:44:19

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF4\01232007\J553459.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:2 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:10 M:283 W: Missing Blank Line separator, <120> field identifier  
L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:283 W: Missing Blank Line separator, <160> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:37 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:40 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:43 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:52 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:55 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:59 M:254 E: No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=1  
L:62 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
L:62 M:112 C: (48) String data converted to lower case,  
L:65 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
M:112 Repeated in SeqNo=1  
L:72 M:252 E: No. of Seq. differs, <211> LENGTH: Input:2259 Found:2269 SEQ:1  
L:78 M:283 W: Missing Blank Line separator, <400> field identifier  
L:87 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:103 M:283 W: Missing Blank Line separator, <400> field identifier  
L:109 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:283 W: Missing Blank Line separator, <400> field identifier  
L:119 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:122 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:125 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:126 M:259 W: Allowed number of lines exceeded, <211> LENGTH:  
L:131 M:283 W: Missing Blank Line separator, <400> field identifier